

FIGURE 1

1 CCCACGCGTCCGGTCCGAGCTAGAGCTCCAAGGACCCACGCCTGTGTCTCTGTGACAGA
61 GCTCAAAGGGCCCTGGGCCCTCCCTCCCTGGCTCGGCTGTGCTTGGGAGGGTTCCCCAGT
121 CCAGAATCCCTAAGGAGCATGGGGCAGCTGATCCATCCCTGGTGTACAAACTGCTGACTG
181 CAGACAGATGCTGAGCTACCCAAACCAACACCTAGCCTCTCCCTGAAGATCCTCCCAGGC
241 TGAGAGAGTTCTGGGTGTCTTAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCA
301 AAGCCCTAACCTGTCCAGCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTTG
361 ATGACAAACCAATTTCCCTCGATGATGTGCTTCTGAGTGCTCTGCTGAGGAACAATGGGA
421 AGTCTGCCCAGCAGAAGAAAATCTCTGCCAAGCCCAAGCTTGAGTTCTCTGTCCAAGGC
481 CAGGGACCTGTGACCATGGAAGCAGAGAGAAGCAAGGCCACAGCCGTGGCCCTGGGCGAGT
541 TTCCCGGCAGGTGGCCCGGCCGAGCTGTGCTGAGACTCGGGGAGCCATTGACCATCGTC
601 TCTGAGGATGGAGACTGGTGGACGGTGTCTGAAGTCTCAGGCAGAGAGTATAACATC
661 CCCAGCGTCCACGTGGCCAAAGTCTCCCATGGGTGGCTGTATGAGGGCCTGAGCAGGGAG
721 AAAGCAGAGGAACCTGCTGTTTACCTGGGAACCCTGGAGGGGCTTCCCTCATCCGGGAG
781 AGCCAGACCAGGAGAGGCTCTTACTCTCTGTCTAGTCCGCCCTCAGCCGCCCTGCATCCTGG
841 GACCGGATCAGACACTACAGGATCCACTGCCCTTGACAATGGCTGGCTGTACATCTCACCG
901 CGCCTCACCTTCCCTCACTCCAGGCCCTGGTGGACCATTACTCTGAGCTGGCGGATGAC
961 ATCTGCTGCCTACTCAAGGAGCCCTGTGTCTCTGCAGAGGGCTGGCCCGCTCCCTGGCAAG
1021 GATATACCCCTACCTGTGACTGTGCAGAGGACACCACTCAACTGGAAGAGCTGGACAGC
1081 TCCCTCCTGTTTTCTGAAGCTGCCACAGGGGAGGAGTCTCTTCTCAGTGAGGGTCTCCGG
1141 GAGTCCCTCAGCTTCTACATCAGCCTGAATGACGAGGCTGTCTCTTTGGATGATGCCTAG
1201 GCCCAAAGGAGAGGGCCAAAAGGGAACCAAGGCTGCACACCTAGAACCCCAATTCAGCCT
1261 CCTGGGCACCCAGAGGCAAGGCTGTGCACCTCAGGGAGGGAGGGTGGGACACAGAGGTGC
1321 ATCTAGGGTCCCACCTGTACCCTTGCTCTTTCCCTCTCTTAGCCCTTAGAAGTCACTACT
1381 TCCTTCCAGTGCCATGATCCCACCTGCGACCTCTAGTGCGAGTGCAGAGAAGGTGGGACC
1441 AGGGCCAGGGTTCCAAAAAGAGAATAAGCCTCCTGGGGGGTCTGACCTAGTTAGTTCTTG
1501 AGTTTGGGGTTTCCAGTACCATCTGGATGCCCTGCCTGTTGAGCCCCATTCTACATCCCC
1561 ACCATTAACCAGGCCCCACCCACAAGGTAGAAACAACCCCTAGAGTCAACGAGAAAGTCA
1621 TTTTCAGAAAATCTACAAGTCTCGTTGAGACCACCACCATAACCTCAGAAGGTAGGACTGT
1681 GGCCTAGAAGGGAAAGGAAAGCTGAGATGATGTCTTACCGTAGCAGCAGATCTTGGATGG
1741 TCCAGGCTCTATGTGACCTCCAGAGCAAAGAGAAAGACTTCGGACAGTCTAGGTCTCTCAA
1801 ATGTCCCCCATTGAGGACAACAGCCCCAGCTCTTTTTCTTTTTTTTTTTTGGACCGAGTCTT
1861 GCCCTGTTGCCCATGCTGGAGTGCAATGGCACGATCTCAGCTCACTGCAACCTCCATCTC
1921 CTGGATTCAAACAATTCTCCTGCCTCAGCCTCCAGAATAGCTGGGATTACAGGCGTACAC
1981 CACCATGCCTGGCTAATTTTTTTGTATTTTTTAGTAGACATGGGGTTTCACCACATTGGCC
2041 AGGCTGGTGTGCAACTCCTGACCTCAGGTGATCCACCCACCTTGGCCTCCCAAAGTGCTG
2101 GGATTACAGGTGTGAGCCACGGCACCCAGCCTAGCTCTCAGATCTCTATTTCATTTTGTG
2161 GCTTACCATTCCCTAGCACACTGGCCTTGCCATCTTGTGGCCGAATAAAAAATAACACCT
2221 CTTAAGTCTAGCACACTGCAGTGAGGCCAGGCACCTCAGTGCTGGGCAGGGGCATCAGAA
2281 GGTGCTAAGCCCTCTCTCCACAATGCCAAGACGGAGACCACAGCCTACACCAAATCCAGC
2341 CCTTGATTTCCCTGCTGCCTCCATAAACAGAAAGAGGTCTGCTGGATCCGCTAAGGGATC
2401 AGGGAGAGGAAGAAAGAGGGATGGGGTGGGAGGCACCCCTCCAGTGCTCCTACTGGTTTC
2461 CCAAGCTACAGGTGGGGTGGGAAAGGCTTTATCAGGTATCATCAACAGGTTCTCAATTAA
2521 AGATTTGATTTATTCAAGTATGTGAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 2

1																			M	G
3	S	L	P	S	R	R	K	S	L	P	S	P	S	L	S	S	S	V	Q	G
23	Q	G	P	V	T	M	E	A	E	R	S	K	A	T	A	V	A	L	G	S
43	F	P	A	G	G	P	A	E	L	S	L	R	L	G	E	P	L	T	I	V
63	S	E	D	G	D	W	W	T	V	L	S	E	V	S	G	R	E	Y	N	I
83	P	S	V	H	V	A	K	V	S	H	G	W	L	Y	E	G	L	S	R	E
103	K	A	E	E	L	L	L	L	P	G	N	P	G	G	A	F	L	I	R	E
123	S	Q	T	R	R	G	S	Y	S	L	S	V	R	L	S	R	P	A	S	W
143	D	R	I	R	H	Y	R	I	H	C	L	D	N	G	W	E	Y	I	S	P
163	R	L	T	F	P	S	L	Q	A	L	V	D	H	Y	S	E	L	A	D	D
183	I	C	C	L	L	K	E	P	C	V	L	Q	R	A	G	P	L	P	G	K
203	D	I	P	L	P	V	T	V	Q	R	T	P	L	N	W	K	E	L	D	S
223	S	L	L	F	S	E	A	A	T	G	E	E	S	L	L	S	E	G	L	R
243	E	S	L	S	F	Y	I	S	L	N	D	E	A	V	S	L	D	D	A	*

FIGURE 3A

1 CCCACGCGTCCGGTCCGAGCTAGAGCTCCAAGGACCCACGCCTGTGTCTCTGTGACAGA
 61 GCTCAAAGGGCCCTGGGCCCTTCCCTCCCTGGCTCGGCTGTGCTTGGGAGGGTTCCCCAGT
 121 CCAGAATCCCTAAGGAGCATGGGGCAGCTGATCCATCCCTGGTGTACAACTGCTGACTG
 181 CAGACAGATGCTGAGCTACCCAAACCAACACCTAGCCTCTCCCTGAAGATCCTCCAGGC
 241 TGAGAGAGTTCTGGGTGTCTTAGGACCAAGGACACTGGCAGACTTCCAGAAGGGCCCCCA
 301 AAGCCCTAACCTGTCCAGCCAGAGCATGCGTCTCAGCAGAGCTGTCTTCCCAAGCCTTTG
 361 ATGACAAACCAATTTCCCTCGATGATGTGCTTCTGAGTGCTCTGCTGAGGAACAATGGGA
 1 M G
 421 AGTCTGCCCAGCAGAAGAAAATCTCTGCCAAGCCCAAGCTTGAGTTCTCTGTCCAAGGC
 3 S L P S R R K S L P S P S L S S S V Q G
 481 CAGGGACCTGTGACCATGGAAGCAGAGAGAAGCAAGGCCACAGCCGTGGCCCTGGGCAGT
 23 Q G P V T M E A E R S K A T A V A L G S
 541 TTCCCGGCAGGTGGCCCCGGCCGAGCTGTGCTGAGACTCGGGGAGCCATTGACCATCGTC
 43 F P A G G P A E L S L R L G E P L T I V
 601 TCTGAGGATGGAGACTGGTGGACGGTGTCTGTCTGAAGTCTCAGGCAGAGAGTATAACATC
 63 S E D G D W W T V L S E V S G R E Y N I
 661 CCCAGCGTCCACGTGGCCAAAGTCTCCCATGGGTGGCTGTATGAGGGCCTGAGCAGGGAG
 83 P S V H V A K V S H G W L Y E G L S R E
 721 AAAGCAGAGGAACCTGCTGTTGTTACCTGGGAACCCCTGGAGGGGCCTTCCTCATCCGGGAG
 103 K A E E L L L L P G N P G G A F L I R E
 781 AGCCAGACCAGGAGAGGCTCTTACTCTCTGTGCTAGTCCGCCTCAGCCGCCCTGCATCCTGG
 123 S Q T R R G S Y S L S V R L S R P A S W
 841 GACCGGATCAGACACTACAGGATCCACTGCCTTGACAATGGCTGGCTGTACATCTCACCG
 143 D R I R H Y R I H C L D N G W L Y I S P
 901 CGCCTCACCTTCCCTCACTCCAGGCCCTGGTGGACCATTAATCTGAGCTGGCGGATGAC
 163 R L T F P S L Q A L V D H Y S E L A D D
 961 ATCTGCTGCCTACTCAAGGAGCCCTGTGTCTGCTGAGAGGGCTGGCCCGCTCCCTGGCAAG
 183 I C C L L K E P C V L Q R A G P L P G K
 1021 GATATACCCCTACCTGTGACTGTGAGAGGACACCACTCAACTGGAAAGAGCTGGACAGC
 203 D I P L P V T V Q R T P L N W K E L D S
 1081 TCCCTCCTGTTTTCTGAAGCTGCCACAGGGGAGGAGTCTCTTCTCAGTGAGGGTCTCCGG
 223 S L L F S E A A T G E E S L L S E G L R
 1141 GAGTCCCTCAGCTTCTACATCAGCCTGAATGACGAGGCTGTCTCTTTGGATGATGCCTAG
 243 E S L S F Y I S L N D E A V S L D D A *
 1201 GCCCAAAGGAGAGGCCAAAAGGAAACCAAGGCTGCACACCTAGAACCCCAATTCAGCCT
 1261 CCTGGGCACCCAGAGGCAAGGCTGTGCACTCAGGGAGGGAGGGTGGGACACAGAGGTGC
 1321 ATCTAGGGTCCACCTGTACCTTGCTCTTTCTCTCTTAGCCCTTAGAAGTCACCTACT
 1381 TCCTTCCAGTGCCATGATCCCACCTGCGACCTCTAGTGCGAGTGCAGAGAAGGTGGGACC
 1441 AGGGCCAGGGTTCCAAAAGAGAATAAGCCTCCTGGGGGGTCTGACCTAGTTAGTTCTTG
 1501 AGTTTGGGGTTTCCAGTACCATCTGGATGCCCTGCCTGTTGAGCCCCATTCTACATCCCC
 1561 ACCATTAACAGGCCCCACCCACAAGGTAGAAACAACCCCTAGAGTCAACGAGAAAGTCA
 1621 TTTTCAGAAAATCTACAAGTCTCGTTGAGACCACCACCATACCTCAGAAGGTAGGACTGT

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FIGURE 3B

1681 GGCCTAGAAGGGAAAGGAAAGCTGAGATGATGTCTTACCGTAGCAGCAGATCTTGGATGG
1741 TCCAGGCTCTATGTGACCTCCAGAGCAAAGAGAAAGACTTCGGACAGTCTAGGTCTCTCAA
1801 ATGTCCCCCATTGAGGACAACAGCCCCAGCTCTTTTTCTTTTTTTTTTGAGACGGAGTCTT
1861 GCCCTGTTGCCCATGCTGGAGTGCAATGGCACGATCTCAGCTCACTGCAACCTCCATCTC
1921 CTGGATTCAAACAATTCTCCTGCCTCAGCCTCCAGAATAGCTGGGATTACAGGCGTACAC
1981 CACCATGCCTGGCTAATTTTTTTTGTATTTTGTAGTAGACATGGGGTTTCACCACATTGGCC
2041 AGGCTGGTGTGCAACTCCTGACCTCAGGTGATCCACCCACCTTGGCCTCCCAAAGTGCTG
2101 GGATTACAGGTGTGAGCCACGGCACCCAGCCTAGCTCTCAGATCTCTATTTTCATTTTGTG
2161 GCTTACCATTCCCTAGCACACTGGCCTTGCCATCTTGTGGCCGAATAAAAAATAACACCT
2221 CTTAAGTCTAGCACACTGCAGTGAGGCCAGGCACCTCAGTGCTGGGCAGGGGCATCAGAA
2281 GGTGCTAAGCCCTCTCTCCACAATGCCAAGACGGAGACCACAGCCTACACCAAATCCAGC
2341 CCTTGATTTCCCTGCTGCCTCCATAAACAGAAAGAGGTCTGCTGGATCCGCTAAGGGATC
2401 AGGGAGAGGAAGAAAGAGGGATGGGGTGGGAGGCACCCCTCCAGTGCTCCTACTGGTTC
2461 CCAAGCTACAGGTGGGGTGGGAAAGGCTTTATCAGGTATCATCAACAGGTCTCAATTAA
2522 AGATTTGATTTATTCAAGTATGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

1681 1741 1801 1861 1921 1981 2041 2101 2161 2221 2281 2341 2401 2461 2522

FIGURE 4

Homology	Amino acid level	
	Similarity	Identity
human SLAP x mouse SLAP	89.9%	88.0%
human SLAP x human SLAP-2	58.4%	47.4%
mouse SLAP x human SLAP-2	70.0%	58.1%

FIGURE 5

hSLAP-2	1	MGSLPSRRKSLPSPSLSSSVQGQGPVTMEAERSKATAVALGSFPAGGP
		: . . : :
hSLAP	1	...MGNSMKSTPAPA.....ERLPNPEGLDSDFLAVLSDYPSPDISP
	51	LSLRLGEPLTIVSEGDWWTVLSEVSGREYNIPSVHVAKVSHGWLYEGLS
		: : : : . : :
	41	PIFRRGEKLRVISDEGGWWKAISLSTGRESYIPGICVARVYHGWLFEGLG
	101	REKAEELLLLPGNPGGAFLIRESQTRRGSYSLSVRLSRPASWDRIRHYRI
		: . : : : : . : :
	91	RDKAEELLQLPDTKVGSFMIRESETKKGFYLSVR.....HRQVKHYRI
	151	HCLDNGWLYISPRLTFPSLQALVDHYSELADDICLLKEPCVLQAGPLP
		: . . : . .
	135	FRLPNNWYISPRLTFQCLEDLVNHYSEVADGLCCVLTPCLTQSTAAPA
	201	GKDIPLPVTVQRTPLNWK...ELDSSLLFSEAATG.EESLLSEGLRESLS
		: : . : : .
	185	VRASSPVTLRQKTVDWRRVSRLQEDPEGTENPLGVDESLSYGLRESIA
	247	FYISLNDEAVSLDDA.....
		: .
	235	SYLSLTSEDNTSFDRKKKSISLMYGGSKRKSSFFSPPYFED

Figure 6

hSLAP 1 MGNSMKSTPAPAERPLPNPEGLDSDFLAVLSDYPSPDISPPIFRRGEKLR
||||||| |.|||| |. |||:|||||||. |||||||||
mSLAP 1 MGNSMKSTSPPSERPLSSSEGLESDFLAVLTDYPSPDISPPIFRRGEKLR

51 VISDEGCWWKAISLSTGRESYIPGICVARVYHGWLFEGLGRDKAEELLQL
||||||| |
51 VISDEGCWWKAISLSTGRESYIPGICVARVYHGWLFEGLGRDKAEELLQL

101 PDKVGSFMIRESETKKGFYSLSVRHRQVKHYRIFRLPNNWYYISPRLTF
|||:||||||| |
101 PDKIGSFMIRESETKKGFYSLSVRHRQVKHYRIFRLPNNWYYISPRLTF

151 QCLEDLVNHYSEVADGLCCVLTTPCLTQSTAAPAVRAS.....SSPVTLR
||||||| |
151 QCLEDLVTHYSEVADGLCCVLTTPCLAQNIPAPTSHPSPECTSPGSPVTLR

196 QKTVDWRRVSRQLQEDPEGTENPLGVDESLSYGLRESIASYLSLTSEDNT
||| |:||||||| |
201 QKTFDWKRVSRLQEGSEGAENPLRVDESLSYGLRESIASYLSLTGDDSS

246 SFDRKKKSISL MYGSKRKSSFFSPPYFED 276
||||||| |:|||| |
251 SFDRKKKSLSLMYTGSKRKSSFFSAPQYFED 281

hSLAP
mSLAP
51
101
151
196
201
246
251

[illegible]**mSLAP**

1 MG.SLPSRRKSLPS..PSLSSSVQGGPVTMEAEERSKATAVALGSFPAGG
||| |: | || | |||| :| :| ||| :|. .
1 MGNMKS..TSPPSERP.LSSS...EG...LE...SDFLAV.LTDYPS..

48 PAELS...LRLGEPLTIVSEDGDWWTVLSEVS.GRE.YNIPSVHVAKVSH
| :| | || | :::|| | :| .| ||| | ||| : ||:| |
36 P.DISPPIFRERGEKLRLVISDEGGWWKAIS.LSTGRESY.IPGICVARVYH

93 GWLYEGLSREKAEELLLLPGNPGGAFIRESQTRRGSYLSVRLSRPASW
||| :||| | :||||| || |. :||| :| :| ||||| |
83 GWLFEGLGRDKAEELLQLPDTKIGSFMIRESETKKGFYSLSVR.HR....

143 DRIRHYRIHCLDNGWLYISPRLTFPSLQALVDHYSELADDICLLKEPCV
. :| ||| | | | ||||| | :| | ||||. || :||. | ||.
128 .QVKHYRIFRLPNWYYISPRLTFQCLEDLVTHYSEVADGLCCVLTPCL

193 LQR..A.....GPL..PGKDIPLPVTV.QRTPLNWKELDSSLLFSEAATG
| | | | || | |||. |:| .|| . | | | . |
177 AQNIPAPTSHSPCTSPGS....PVTLRQKT.FDWKRV.SRL..QESEG

233 .E.....ESLLSEGLRESLSFYISL.NDEAVSLD
| | | | ||||| :. |:| | :. | |
219 AENPLRVDESLSFSYGLRESIASYLSLTGDDSSSFD

FIGURE 8

